

POLYPEPTIDE VARIANTS WITH ALTERED EFFECTOR FUNCTION

APPROVED

POLYPEPTIDE VARIANTS WITH ALTERED EFFECTOR FUNCTION

Docket No. P1726R1 3/21 - K322A - P329A - P331A O.G. FIG. 4 APPROVED DRAFTSMAN × 3.5 × 3 2.5 OD (492-405) nm 2 × 1.5 0.5 0 100 80 20 60 40 Concentration of antibody in ($\mu g/mL$) FIG._3

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Serial No. 09/483,588

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APPROVED O.G. FIG.

BY CLASS SUBCLASS

DRAFTSMAN

(E27) - Light Chain

THOGLSSPVT GVPSRFSGSG SGTASVVCLL IFPPSDEQLK EKHKVYACEV LIYAASYLES KRTVAAPSVF QQKPGKAPKL STLTLSKADY GEGDSYMINY DSKDSTYSLS TFGQGTKVEI YCQQSHEDPY GNSQESVTEQ ITCRASKPVD LSASVGDRVT **QWKVDNALQS** SLOPEDFATY NNFYPREAKV DIQLTQSPSS SGTDFTLTIS KSFNRGEC

:1G._4A

(E27) - Heavy Chain

SKAKGOPREP YSKLTVDKSR SHEDPEVKFN TYICHVNHKP PLAPSSKSTS NPSVKGRITI SIKYSGETKY VLDSDGSFFL PEVTCVVVDV SASTKGPSVF TVPSSSLGTQ ALPAPIEKTI KEYKCKVSNK PENNYKTTPP PKDTLMISRT SGLYSLSSVV APGKGLEWVA WGQGTLVTVS IAVEWESNGQ GPSVFLFPPK TVLHQDWLNG HYFGHWHFAV VHTFPAVLQS SGYSWNWIRO × SWNSGALTSG NSTYRVVSVL TOKSLSLSPG PPCPAPELLG CLVKGFYPSD TAVYYCARGS SCAVSGYSIT EMTKNQVSLT VMHEALHNHY LVQPGGSLRL PKSCDKTHTC LOMNSLRAED KDYFPEPVTV AKTKPREEQY WOOGNVFSCS WYVDGVEVHIN EVQLVESGGG GGTAALGCLV SNTKVDKKVE QVYTLPPSRE SRDDSKNTFY

FIG._4B

ALTERED EFFECTOR FUNCTION

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APPROVED O.G. FIG.

BY CLASS SUBCLASS

DRAFTSMAN

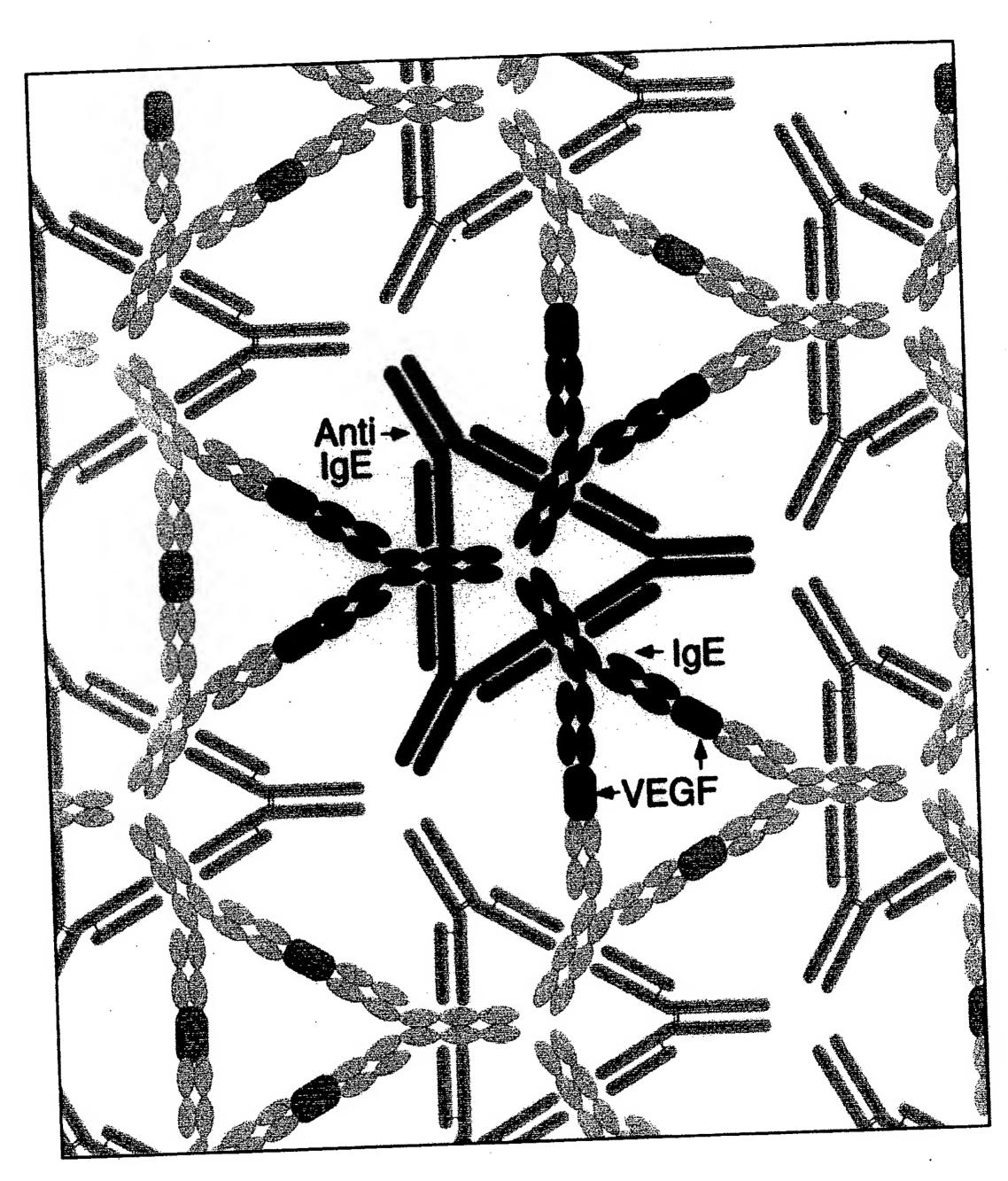


FIG._5

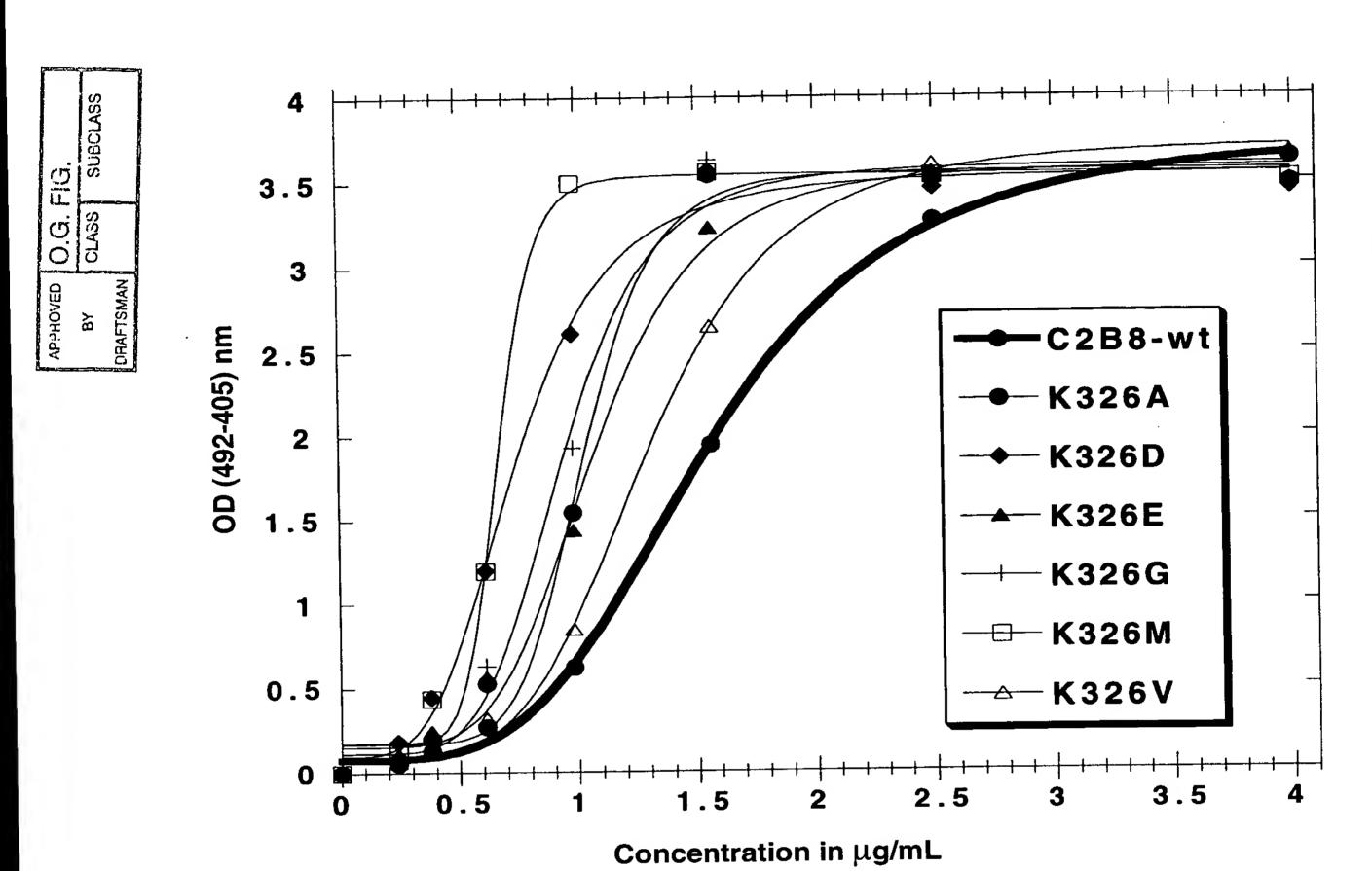


FIG._9

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ALTERED EFFECTOR FUNCTION

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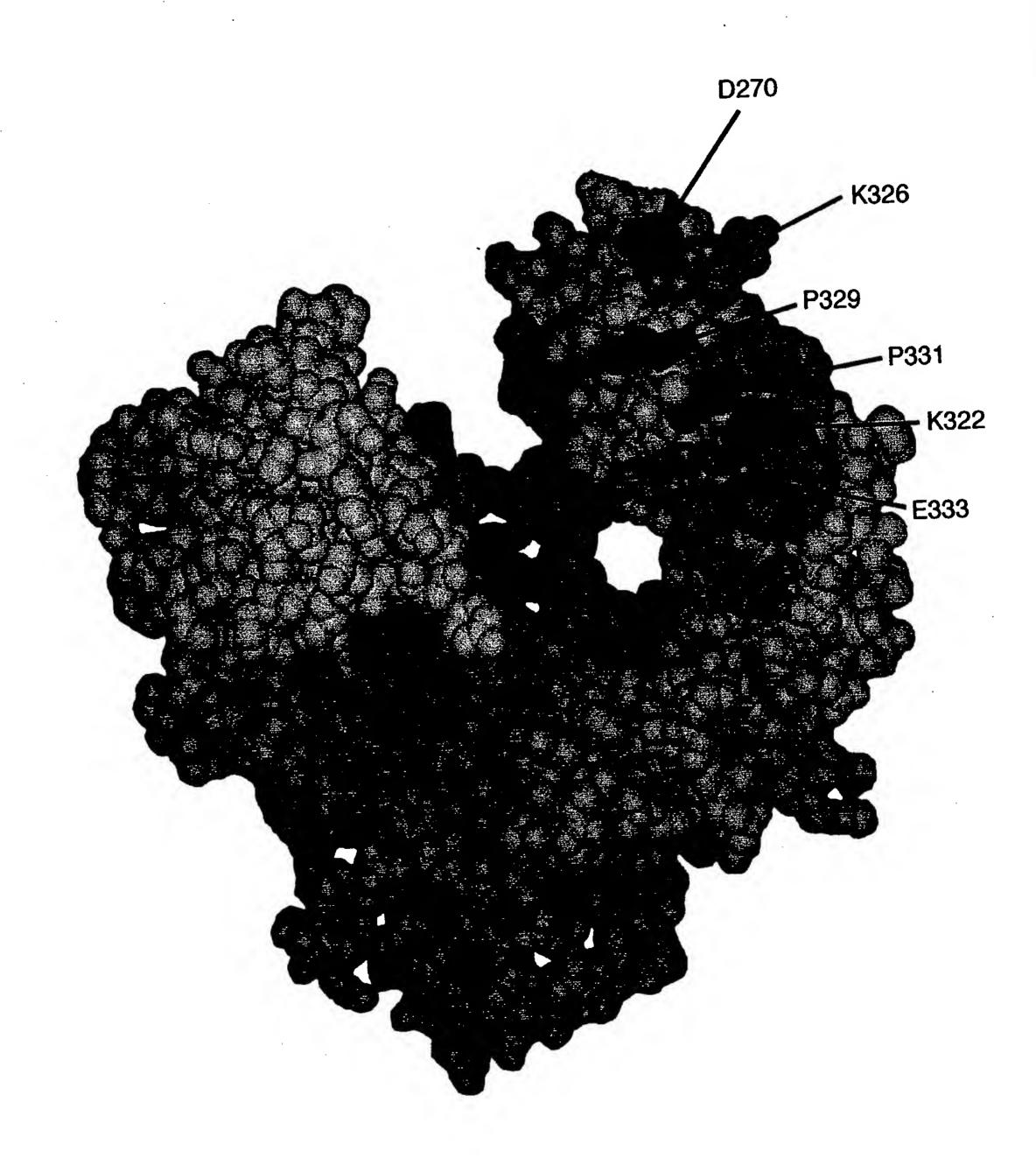


FIG._10

POLYPEPTIDE VARIANTS WITH ALTERED EFFECTOR FUNCTION
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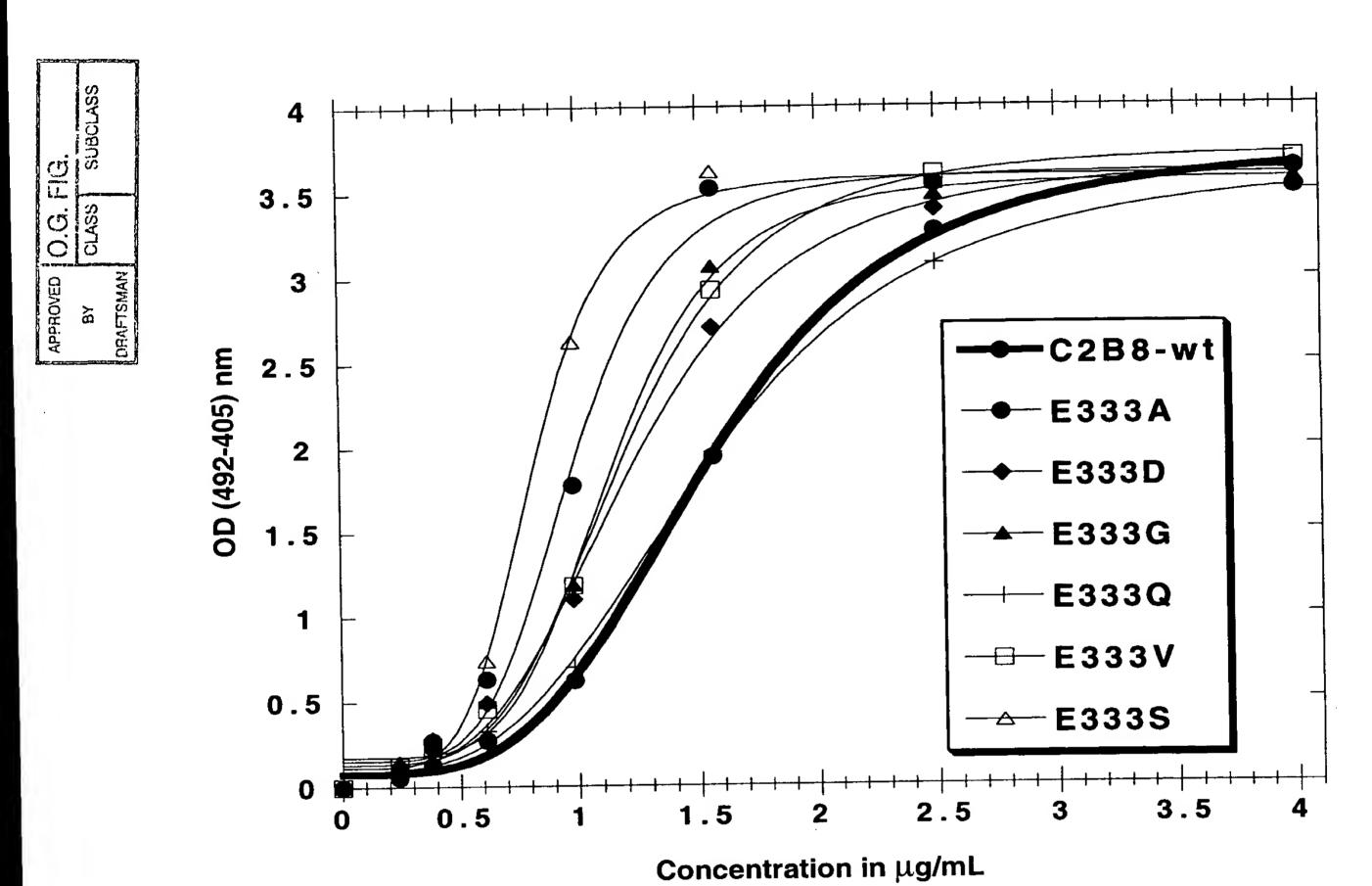


FIG._11

POLYPEPTIDE VARIANTS WITH ALTERED EFFECTOR FUNCTION Leonard Presta Serial No. 09/483,588 Docket No. P1726R1

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APPLOVED O.C. FIG.

BY CLASS SUBCLASS

DRAFTSMAN

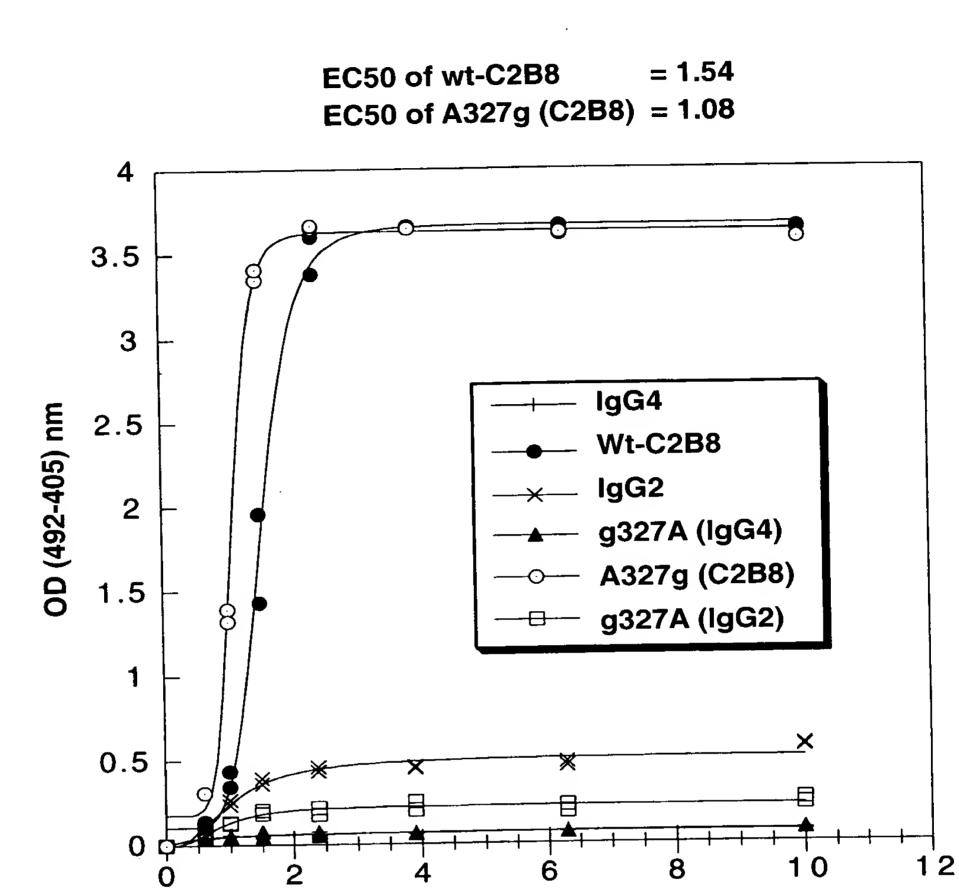


FIG._14

Concentration in $\mu g/mL$

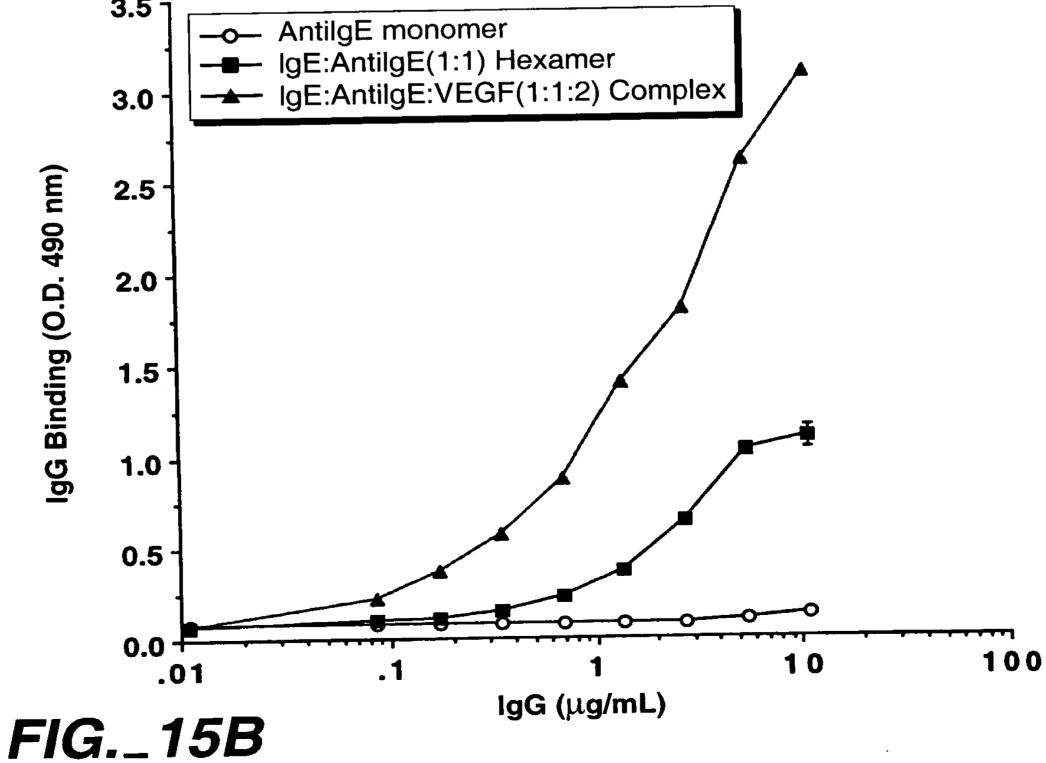


FIG._16B

FIG._18B

FIG._19B

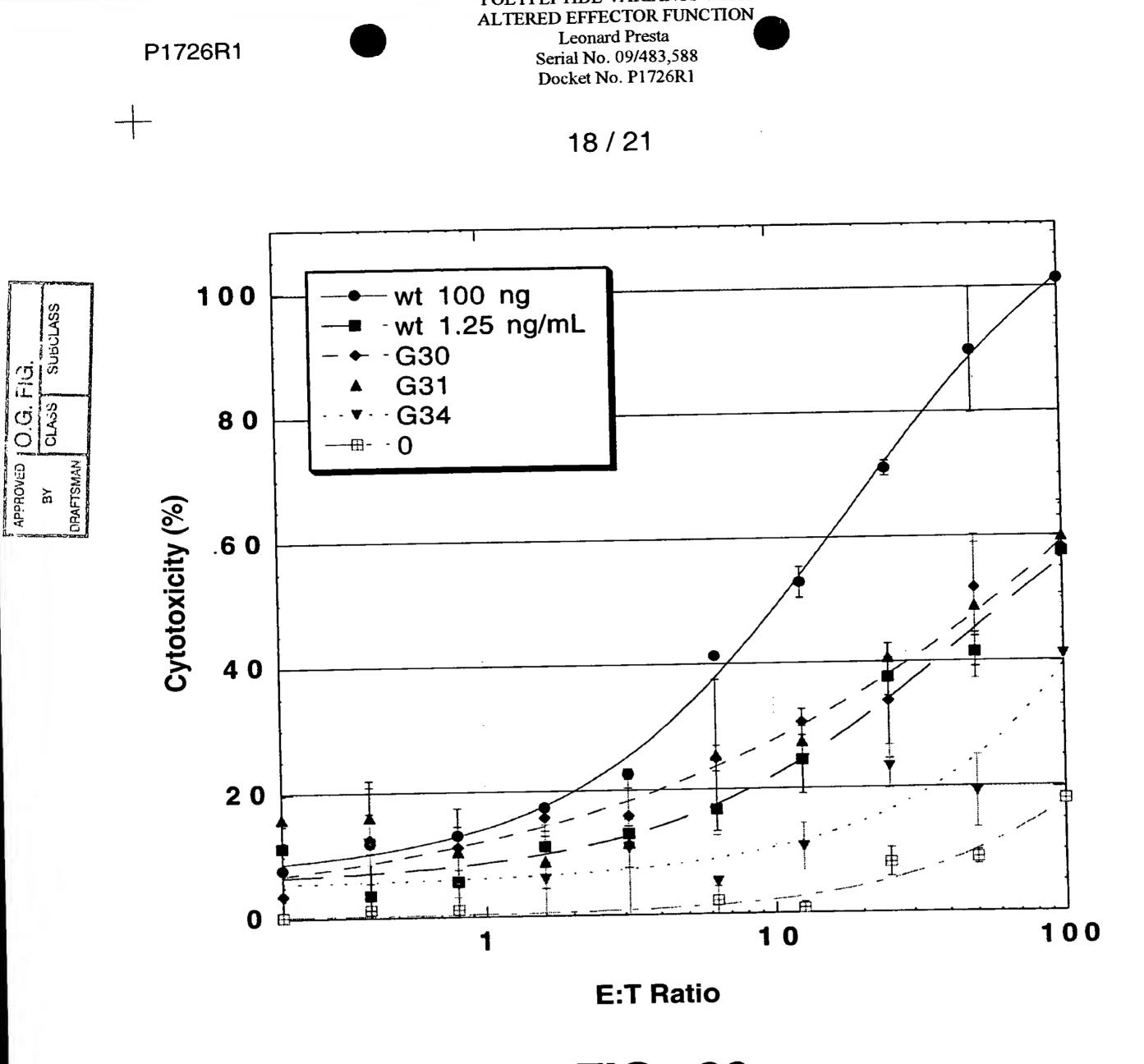


FIG._20

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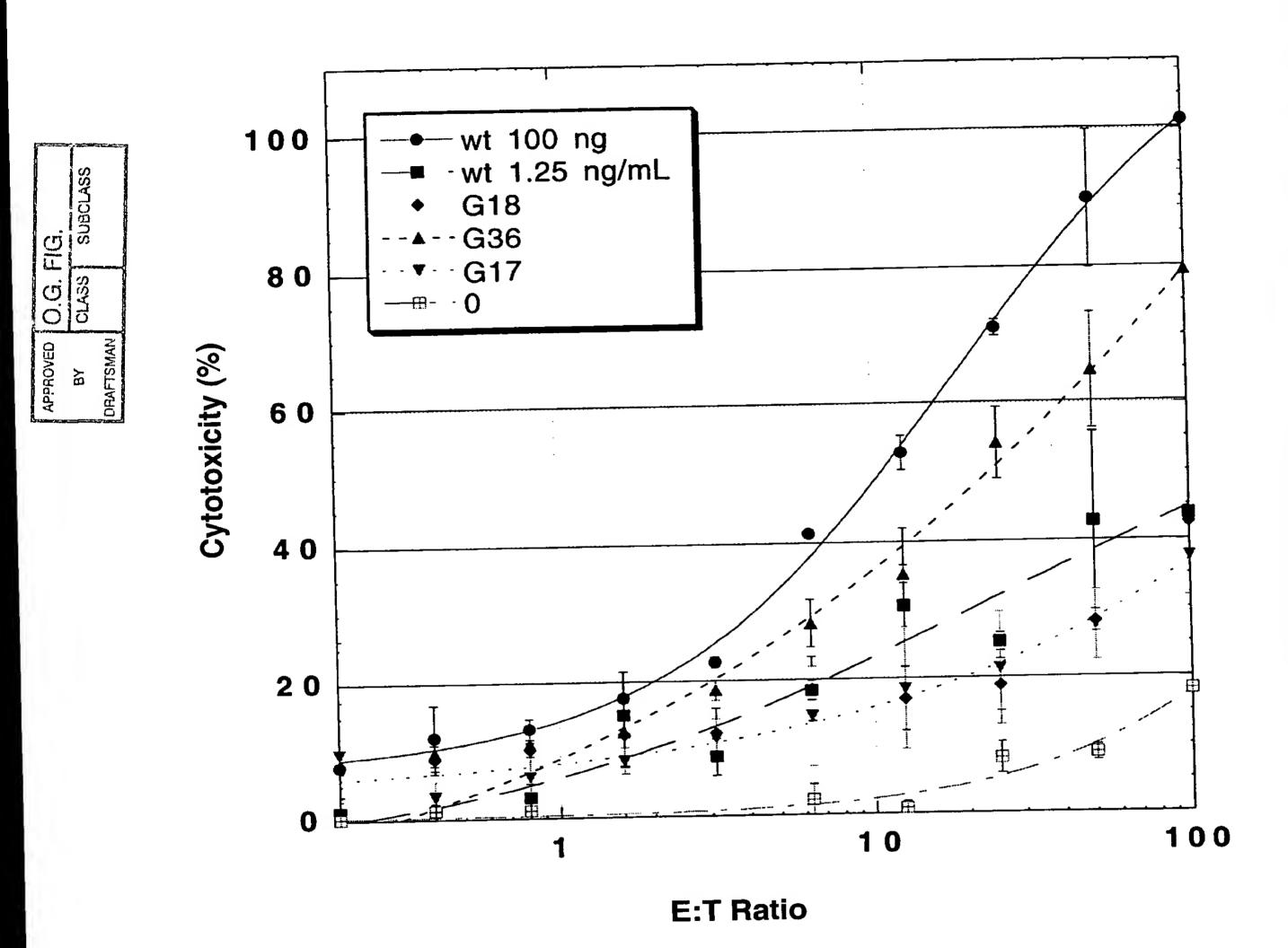


FIG._21

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humIgG1 humIgG2 humIgG3 humIgG4 murIgG1 murIgG2A murIgG2B murIgG3	PAPELLGGPS PAPELLGGPS PAPELLGGPS PAPEFLGGPSTVPEVSS PAPNLLGGPS	SVFLFPPKPKI SVFLFPPKPKI SVFLFPPKPKI SVFIFPPKPKI SVFIFPPKIKI	TLMISRTPEVOTLMISRTPEVOTLMISRTPEVOTLMISRTPEVOTLMISRTPEVOTLMISRTPEVOTLTITLTPKVOVLMISLSPIVOVLMISLTPKV	TCVVVDVSI TCVVVDVSI TCVVVDVSI TCVVVDVSI TCVVVDVSI TCVVVDISI TCVVVDISI	EDPEVKFNWYV EDPEVQFNWYV EDPEVQFKWYV EDPEVQFNWYV CDPEVQFSWFV EDDPDVQISWFV EDDPDVQISWFV EDDPDVVSWFV
humIgG1 humIgG2 humIgG3 humIgG4 murIgG1 murIgG2A murIgG2B murIgG3	DGVEVHNAK DGVEVHNAK DGVEVHNAK DGVEVHNAK DDVEVHTAQ NNVEVHTAQ	TKPREEQFNS' TKPREEQFNS' TKPREEQFNS' TQPREEQFNS' TQTHREDYNS'	TYRVVSVLTV TFRVVSVLTV TFRVVSVLTV TYRVVSVLTV TFRSVSELPI TLRVVSALPI TIRVVSHLPI	LHQDWLNGK VHQDWLNGK LHQDWLNGK LHQDWLNGK MHQDCLNGK QHQDWMSGK QHQDWMSGK	EYKCKVSNKALP EYKCKVSNKGLP EYKCKVSNKALP EYKCKVSNKGLP EYKCKVSNKGLP EFKCRVNSAAFP EFKCKVNNKDLP EFKCKVNNKDLP
humIgG1 humIgG2	APIEKTISK	AKGOPREPOV	YTLPPSREEM D L YTLPPSREEM	TKNQVSLTC	370 LVKGFYPSDIAV LVKGFYPSDIAV
humIgG3 humIgG4 murIgG1 murIgG2A murIgG2B murIgG3	APIEKTISK SSIEKTISK APIEKTISK APIERTISK	TKGQPREPQV AKGQPREPQV TKGRPKAPQV PKGSVRAPQV	YTLPPSREEM YTLPPSQEEM YTIPPPKEQM YVLPPPEEEM YTLPPPAEOL	TKNQVSLTC TKNQVSLTC AKDKVSLTC TKKQVTLTC SRKDVSLTC	LVKGFYPSDIAV LVKGFYPSDIAV MITDFFPEDITV MVTDFMPEDIYV LVVGFNPGDISV LVTNFFSEAISV
humIgG1 humIgG2 humIgG3 humIgG4 murIgG1 murIgG24 murIgG24	EWESNGQPI EWESNGQPI EWESSGQPI EWZSNGQPI EWQWNGQPI EWTNNGKTI	ENNYKTTPPVI ENNYKTTPPMI ENNYNTTPPMI ENNYKTTPPVI AENYKNTQPIM ELNYKNTEPVI	DSDGSFFLYS DSDGSFFLYS DSDGSFFLYS DTDGSYFVYS DSDGSYFMYS	KLTVDKSRV KLTVDKSRV KLTVDKSRV KLTVDKSRV KLTVDKSRV KLNVQKSNV KLRVEKKNV	420 IQQGNVFSCSVMH IQQGNVFSCSVMH IQQGNIFSCSVMH IQEGNVFSCSVMH VEAGNTFTCSVLH IVERNSYSCSVVH VEKTDSFSCNVRH ILQGEIFTCSVVH
humIgG1 humIgG2 humIgG3 humIgG4 murIgG1 murIgG22 murIgG23	EALHNHYTO EALHNHYTO EALHNRFTO EALHNHYTO EGLHNHHTO EGLHNHHTO EGLHNHHTO EGLKNYYL	440 QKSLSLSPGK QKSLSLSPGK QKSLSLSPGK QKSLSLSLGK EKSLSHSPGK TKSFSRTPGK KKTISRSPGK QKNLSRSPGK		FIG	22A

APPROVED O.G. FIG.

BY CLASS SUBCLASS
DRAFTSMAN

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O.G. FIG.

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DRAFTSMAN

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Percent Identity Among Fc Sequences

1.	humIgG1	1	2 94	3 94	4 94	5 64	6 66	7 63	8 68
2.	humIgG2		-	93	92	65	63	60	67
3.	humIgG3			-	91	64	64	61	67
4.	humIgG4				_	62	64	61	64
	murIgG1						65	61	67
6.	murIgG2A						-	77	70
7	murIgG2B							-	68
8.	murIgG3								-

FIG._22B

humIgG1 humIgG2 humIgG3 humIgG4	230 240 250 260 270 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV PAP-PVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYV PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYV PAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYV ****
humIgG1 humIgG2 humIgG3 humIgG4	280 290 300 310 320 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP DGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLP DGVEVHNAKTKPREEQFNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALP DGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLP * * * * * * * *
humIgG1 humIgG2 humIgG3 humIgG4	330 340 350 360 370 APIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV D L APIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV APIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV SSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAV **
humIgG1 humIgG2 humIgG3 humIgG4	390 400 410 420 EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH EWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH EWESSGQPENNYNTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMH EWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMH * * * *
humIgG1 humIgG2 humIgG3 humIgG4	430 440 EALHNHYTQKSLSLSPGK EALHNHYTQKSLSLSPGK EALHNHYTQKSLSLSPGK EALHNHYTQKSLSLSLGK **